```
============================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Keisha Douglas
Timestamp: [year=2008; month=2; day=5; hr=14; min=17; sec=45; ms=80; ]
============================================================



************************************************************
Reviewer Comments:
<210>    7
<211>    54
<212>    DNA
<213>    Oligonucleotide Primer CF59

<400>    7
cgatagatct ttggataaga gagggccacc acctggcccc cctcgagttt cccc          54


 The above <213> response is invalid, also similar responses were found
in sequence id#'s 10 and 11. FYI, these responses can be inserted into
section <220> to <223>.



************************************************************
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Validated By CRFValidator v 1.0.3

Application No: 10584438   Version No: 1.0

Input Set:

Output Set:

                Started: 2008-01-29 15:17:14.169
               Finished: 2008-01-29 15:17:15.923
                Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 754 ms
         Total Warnings: 20
           Total Errors: 1
     No. of SeqIDs Defined: 20
       Actual SeqID Count: 20

Error code	Error Description
E 287	Invalid WIPO ST.2 date format; Use (YYYY-MM-DD) in <141>
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)

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                    Input Set:


                    Output Set:



                    Started:   2008-01-29 15:17:14.169
                    Finished:  2008-01-29 15:17:15.923
                    Elapsed:   0 hr(s) 0 min(s) 1 sec(s) 754 ms
            Total Warnings:    20
              Total Errors:    1
     No. of SeqIDs Defined:    20
        Actual SeqID Count:    20

Error code      Error Description

W   213         Artificial or Unknown found in <213>  in SEQ ID (20)
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<210>   1
<211>   48
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Oligonucleotide Linker VC053

<400>   1
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<210>   2
<211>   50
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Oligonucleotide Linker VC054

<400>   2
ccttgaaccg gtgagcgact tcggacttgt gagcgtctct cttatccaaa   50

<210>   3
<211>   48
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Oligonucleotide Linker VC055

<400>   3
gatctttgga taagagagac gctcacaagt ccgaagtcgc tcatcgat   48

<210>   4
<211>   50
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Oligonucleotide Linker VC056

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<210>   5
<211>   86
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Oligonucleotide Linker VC057

<400>   5
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tgcaacaatg tccattcgaa gatcac   86

<210>   6

<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Linker VC058

<400> 6
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<210> 7
<211> 54
<212> DNA
<213> Oligonucleotide Primer CF59

<400> 7
cgatagatct ttggataaga gagggccacc acctggcccc cctcgagttt cccc   54

<210> 8
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide linker SEQ ID 8

<400> 8
Gly Gly Gly Gly Ser
1   5

<210> 9
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide linker SEQ ID 9

<400> 9
Gly Gly Gly Ser
1

<210> 10
<211> 17
<212> PRT
<213> Stanniocalcin signal peptide sequence

<400> 10
Met Leu Gln Asn Ser Ala Val Leu Leu Leu Leu Val Ile Ser Ala Ser
1   5   10   15

Ala

<210> 11
<211> 22

<212>   PRT
<213>   Consensus signal sequence

<400>   11
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1   5   10   15

Trp Ala Pro Ala Arg Gly
            20

<210>   12
<211>   66
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Oligonucleotide Primer CF60

<400>   12
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cccctc   66

<210>   13
<211>   50
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Oligonucleotide Primer CF61

<400>   13
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<210>   14
<211>   45
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Oligonucleotide Primer CF62

<400>   14
ggccaagctt attacagccg agtcttcagc agcagcagtc ccctc   45

<210>   15
<211>   2358
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   N-terminal IL11-albumin fusion

<400>   15
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ctggacagca ccgtgctcct gacccgctct ctcctggcgg acacgcggca gctggctgca   180
cagctgaggg acaaattccc agctgacggg accacaacc tggattccct gcccacccctg   240

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ctgaagaccc tggagcccga gctgggcacc ctgcaggccc gactggaccg gctgctgcgc    420
cggctgcagc tcctgatgtc ccgcctggcc ctgcccagc caccccggga cccgccggcg    480
ccccgctgg cgcccccctc ctcagctgg ggggggcatca gggccgccca cgccatcctg    540
gggggggctgc acctgacact tgactggggcc gtgaggggac tgctgctgct gaagactcgg    600
ctggacgctc acaagtccga agtcgctcat cgattcaagg acctaggtga ggaaaacttc    660
aaggctttgg tcttgatcgc tttcgctcaa tacttgcaac aatgtccatt cgaagatcac    720
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gaatgtttct tgcaacacaa ggacgacaac ccaaacttgc caagattggt tagaccagaa    960
gttgacgtca tgtgtactgc tttccacgac aacgagaaa ccttcttgaa gaagtacttg   1020
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tgttgtgctg ctgctgaccc acacgaatgt tacgctaagg ttttcgatga attcaagcca   1740
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gaatacaagt ccaaaacgc tttgttggtt agatacacta gaaggtccc acaagtctcc   1860
accccaactt tggttgaagt ctctagaaac ttgggtaagg tcggttctaa gtgttgtaag   1920
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caagctgctt tgggtttg                                                 2358


<210>    16
<211>    786
<212>    PRT
<213>    Artificial Sequence

<220>
<223>    N-terminal IL11-albumin fusion

<400>    16
Met Lys Trp Val Phe Ile Val Ser Ile Leu Phe Leu Phe Ser Ser Ala
1               5                   10                  15


Tyr Ser Arg Ser Leu Asp Lys Arg Gly Pro Pro Pro Gly Pro Pro Arg
            20                  25                  30


Val Ser Pro Asp Pro Arg Ala Glu Leu Asp Ser Thr Val Leu Leu Thr
        35                  40                  45


Arg Ser Leu Leu Ala Asp Thr Arg Gln Leu Ala Ala Gln Leu Arg Asp
    50                  55                  60
```

Lys Phe Pro Ala Asp Gly Asp His Asn Leu Asp Ser Leu Pro Thr Leu
65   70   75   80

Ala Met Ser Ala Gly Ala Leu Gly Ala Leu Gln Leu Pro Gly Val Leu
                85   90   95

Thr Arg Leu Arg Ala Asp Leu Leu Ser Tyr Leu Arg His Val Gln Trp
        100   105   110

Leu Arg Arg Ala Gly Gly Ser Ser Leu Lys Thr Leu Glu Pro Glu Leu
        115   120   125

Gly Thr Leu Gln Ala Arg Leu Asp Arg Leu Leu Arg Arg Leu Gln Leu
    130   135   140

Leu Met Ser Arg Leu Ala Leu Pro Gln Pro Pro Pro Asp Pro Pro Ala
145   150   155   160

Pro Pro Leu Ala Pro Pro Ser Ser Ala Trp Gly Gly Ile Arg Ala Ala
                165   170   175

His Ala Ile Leu Gly Gly Leu His Leu Thr Leu Asp Trp Ala Val Arg
                180   185   190

Gly Leu Leu Leu Leu Lys Thr Arg Leu Asp Ala His Lys Ser Glu Val
        195   200   205

Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val
    210   215   220

Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His
225   230   235   240

Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala
                245   250   255

Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly
                260   265   270

Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met
        275   280   285

Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu
    290   295   300

Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu
305   310   315   320

Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu
                325   330   335

Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala
        340   345   350

Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu
        355   360   365

Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp
    370   375   380

Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys
385   390   395   400

Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala
                405   410   415

Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val
            420   425   430

Ser Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His
    435   440   445

Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr
    450   455   460

Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys
465   470   475   480

Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn
                485   490   495

Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu
            500   505   510

Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu
    515   520   525

Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val
    530   535   540

Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys
545   550   555   560

Cys Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp
            565   570   575

Glu Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn
            580   585   590

Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu
    595   600   605

Leu Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu
    610   615   620

Val Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys
625   630   635   640

His Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val
            645   650   655

Val Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp
            660   665   670

```
Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys
        675                 680                 685

Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn
        690                 695                 700

Ala Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys
705                 710                 715                 720

Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His
                725                 730                 735

Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe
                740                 745                 750

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys
        755                 760                 765

Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu
        770                 775                 780

Gly Leu
785


<210>    17
<211>    762
<212>    PRT
<213>    Artificial Sequence

<220>
<223>    Mature N-terminal IL11-albumin fusion

<400>    17
Gly Pro Pro Pro Gly Pro Pro Arg Val Ser Pro Asp Pro Arg Ala Glu
1                 5                   10                  15

Leu Asp Ser Thr Val Leu Leu Thr Arg Ser Leu Leu Ala Asp Thr Arg
                20                  25                  30

Gln Leu Ala Ala Gln Leu Arg Asp Lys Phe Pro Ala Asp Gly Asp His
        35                  40                  45

Asn Leu Asp Ser Leu Pro Thr Leu Ala Met Ser Ala Gly Ala Leu Gly
        50                  55                  60

Ala Leu Gln Leu Pro Gly Val Leu Thr Arg Leu Arg Ala Asp Leu Leu
65                  70                  75                  80

Ser Tyr Leu Arg His Val Gln Trp Leu Arg Arg Ala Gly Gly Ser Ser
                85                  90                  95

Leu Lys Thr Leu Glu Pro Glu Leu Gly Thr Leu Gln Ala Arg Leu Asp
                100                 105                 110

Arg Leu Leu Arg Arg Leu Gln Leu Leu Met Ser Arg Leu Ala Leu Pro
        115                 120                 125
```

Gln Pro Pro Pro Asp Pro Pro Ala Pro Pro Leu Ala Pro Pro Ser Ser
130   135   140

Ala Trp Gly Gly Ile Arg Ala Ala His Ala Ile Leu Gly Gly Leu His
145   150   155   160

Leu Thr Leu Asp Trp Ala Val Arg Gly Leu Leu Leu Lys Thr Arg
            165   170   175

Leu Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly
            180   185   190

Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu
            195   200   205

Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr
    210   215   220

Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp
225   230   235   240

Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr
            245   250   255

Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu
            260   265   270

Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn
            275   280   285

Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe
    290   295   300

His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala
305   310   315   320

Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys
            325   330   335

Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala
            340   345   350

Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala
    355   360   365

Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly
    370   375   380

Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe
385   390   395   400

Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr
            405   410   415

Lys Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp
            420   425   430

Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile
        435   440   445

Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser
        450   455   460

His Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro
465   470   475   480

Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr
                485   490   495

Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala
            500   505   510

Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys
        515   520   525

Thr Tyr Glu Thr Thr Leu Glu Lys Cys